



PCT10

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,143

DATE: 08/29/2002

TIME: 14:03:31

Input Set : A:\271_294.ST25.txt

Output Set: N:\CRF3\08292002\J088143.raw

3 <110> APPLICANT: PESTKA, Sidney
 4 KOTENKO, Sergei
 6 <120> TITLE OF INVENTION: Cytomegalovirus-Encoded IL-10 Homolog
 8 <130> FILE REFERENCE: 271/294
 10 <140> CURRENT APPLICATION NUMBER: 10/088,143
 11 <141> CURRENT FILING DATE: 2002-02-22
 13 <150> PRIOR APPLICATION NUMBER: PCT/US00/24213
 14 <151> PRIOR FILING DATE: 1999-09-02
 16 <150> PRIOR APPLICATION NUMBER: 60/152,062
 17 <151> PRIOR FILING DATE: 1999-09-02
 19 <160> NUMBER OF SEQ ID NOS: 21
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 789
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Cytomegalovirus
 28 <400> SEQUENCE: 1

29	cagttggcg	gcggactggg	acggcatgtc	gcggcgatgc	tgtcggtgat	ggtctttcc	60									
31	tctctgtcc	tgatcgctt	ttttctaggc	gcttcggagg	aggcgaagcc	ggcgacgacg	120									
33	acgataaaga	atacaaagcc	gcagtgtcg	ccagaggatt	acgcgaccag	attgcaagat	180									
35	ctccgcgtca	ccttcatcg	agtaaaacct	acgttggtag	gtcacgtagg	tacggtttat	240									
37	tgcgacggtc	tttctttcc	gcgtgtcggg	tgacgtagtt	ttccttctgt	agcaacgtga	300									
39	ggacgactac	tccgtgtggc	tcgacggta	ggtgtcaaa	ggctgttggg	gatgcagcgt	360									
41	catggactgg	ttgttggaggc	ggtatctgga	gatcggttt	ccgcaggcg	accacgtcta	420									
43	tcccgactc	aagacgaaat	tgcatagtt	gcgcgtcgacg	ctagaatcca	tctacaaaga	480									
45	catgcccaca	tgttaagtg	tctctgtggc	ggcgctgtcc	gcacagaggt	aacaacgtgt	540									
47	tcatagcact	ctgtttact	tttgcggggc	tcccagccct	tgttaggtt	cgagataag	600									
49	tccgtgatta	gtcggctgtc	tcaggaggcg	gaaaggaaat	cgataacgg	cacgcggaaa	660									
51	ggtctcagcg	agttggacac	gttgttttagc	cgtctcgaag	agtatctgca	ctcgagaaaag	720									
53	tagcgttgcg	atttgcagtc	cgctccgggt	tcgttcaccc	agttacttta	ataaacgtac	780									
55	tgttaacc						789									
58	<210>	SEQ ID NO:	2													
59	<211>	LENGTH:	175													
60	<212>	TYPE:	PRT													
61	<213>	ORGANISM:	Cytomegalovirus													
63	<400>	SEQUENCE:	2													
65	Met	Leu	Ser	Val	Met	Val	Ser	Ser	Ser	Leu	Val	Ile	Val	Phe	Phe	
66	1				5					10				15		
69	Leu	Gly	Ala	Ser	Glu	Glu	Ala	Lys	Pro	Ala	Thr	Thr	Thr	Ile	Lys	Asn
70					20					25				30		
73	Thr	Lys	Pro	Gln	Cys	Arg	Pro	Glu	Asp	Tyr	Ala	Thr	Arg	Leu	Gln	Asp
74					35					40				45		
77	Leu	Arg	Val	Thr	Phe	His	Arg	Val	Lys	Pro	Thr	Leu	Gln	Arg	Glu	Asp

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78 50 55 60
81 Asp Tyr Ser Val Trp Leu Asp Gly Thr Val Val Lys Gly Cys Trp Gly
82 65 70 75 80
85 Cys Ser Val Met Asp Trp Leu Leu Arg Arg Tyr Leu Glu Ile Val Phe
86 85 90 95
89 Pro Ala Gly Asp His Val Tyr Pro Gly Leu Lys Thr Glu Leu His Ser
90 100 105 110
93 Met Arg Ser Thr Leu Glu Ser Ile Tyr Lys Asp Met Arg Gln Cys Pro
94 115 120 125
97 Leu Leu Gly Cys Gly Asp Lys Ser Val Ile Ser Arg Leu Ser Gln Glu
98 130 135 140
101 Ala Glu Arg Lys Ser Asp Asn Gly Thr Arg Lys Gly Leu Ser Glu Leu
102 145 150 155 160
105 Asp Thr Leu Phe Ser Arg Leu Glu Glu Tyr Leu His Ser Arg Lys
106 165 170 175
109 <210> SEQ ID NO: 3
110 <211> LENGTH: 25
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: synthetic sequence
117 <400> SEQUENCE: 3
118 tcctacagaa actattctaa ccgcg 25
121 <210> SEQ ID NO: 4
122 <211> LENGTH: 25
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: synthetic sequence
129 <400> SEQUENCE: 4
130 tcatctttcc agccgccta gcaac 25
133 <210> SEQ ID NO: 5
134 <211> LENGTH: 25
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: synthetic sequence
141 <400> SEQUENCE: 5
142 catcataaca taaaggacca cctac 25
145 <210> SEQ ID NO: 6
146 <211> LENGTH: 25
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: synthetic sequence
153 <400> SEQUENCE: 6
154 cgacgcacac tggtaaaca gtacg 25
157 <210> SEQ ID NO: 7
158 <211> LENGTH: 25

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159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: synthetic sequence
165 <400> SEQUENCE: 7
166 gggacggcat gctgccccga tgctg 25
169 <210> SEQ ID NO: 8
170 <211> LENGTH: 25
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial sequence
174 <220> FEATURE:
175 <223> OTHER INFORMATION: synthetic sequence
177 <400> SEQUENCE: 8
178 agtaactggg tgaacgacac cggag 25
181 <210> SEQ ID NO: 9
182 <211> LENGTH: 25
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: synthetic sequence
189 <400> SEQUENCE: 9
190 aggcgcttcc gaggaggcga agccg 25
193 <210> SEQ ID NO: 10
194 <211> LENGTH: 25
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: synthetic sequence
201 <400> SEQUENCE: 10
202 gactgcaaat cgcaacgcta ctttc 25
205 <210> SEQ ID NO: 11
206 <211> LENGTH: 24
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: synthetic sequence
213 <400> SEQUENCE: 11
214 taggatcctt ccgaggaggc gaag 24
217 <210> SEQ ID NO: 12
218 <211> LENGTH: 20
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: synthetic sequence
225 <400> SEQUENCE: 12
226 atgaattcggt tgttacctct 20
229 <210> SEQ ID NO: 13
230 <211> LENGTH: 22
231 <212> TYPE: DNA

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232 <213> ORGANISM: Artificial sequence
 234 <220> FEATURE:
 235 <223> OTHER INFORMATION: synthetic sequence
 237 <400> SEQUENCE: 13
 238 agcggaaattc aaatcgcaac gc 22
 241 <210> SEQ ID NO: 14
 242 <211> LENGTH: 27
 243 <212> TYPE: DNA
 244 <213> ORGANISM: Artificial sequence
 246 <220> FEATURE:
 247 <223> OTHER INFORMATION: synthetic sequence
 249 <400> SEQUENCE: 14
 250 cgggatccca gcccaggcga gggcacc 27
 253 <210> SEQ ID NO: 15
 254 <211> LENGTH: 26
 255 <212> TYPE: DNA
 256 <213> ORGANISM: Artificial sequence
 258 <220> FEATURE:
 259 <223> OTHER INFORMATION: synthetic sequence
 261 <400> SEQUENCE: 15
 262 gctctagatc agtttcgtat cttcat 26
 265 <210> SEQ ID NO: 16
 266 <211> LENGTH: 21
 267 <212> TYPE: DNA
 268 <213> ORGANISM: Artificial sequence
 270 <220> FEATURE:
 271 <223> OTHER INFORMATION: synthetic sequence
 273 <400> SEQUENCE: 16
 274 cgggatcctg cggcgatgct g 21
 277 <210> SEQ ID NO: 17
 278 <211> LENGTH: 22
 279 <212> TYPE: DNA
 280 <213> ORGANISM: Artificial sequence
 282 <220> FEATURE:
 283 <223> OTHER INFORMATION: synthetic sequence
 285 <400> SEQUENCE: 17
 286 agcggaaattc aaatcgcaac gc 22
 289 <210> SEQ ID NO: 18
 290 <211> LENGTH: 78
 291 <212> TYPE: PRT
 292 <213> ORGANISM: Cytomegalovirus
 294 <400> SEQUENCE: 18
 296 Met Leu Ser Val Met Val Ser Ser Ser Leu Val Leu Ile Val Phe Phe
 297 1 5 , 10 15
 300 Leu Gly Ala Ser Glu Glu Ala Lys Pro Ala Thr Thr Thr Ile Lys Asn
 301 20 25 30
 304 Thr Lys Pro Gln Cys Arg Pro Glu Asp Tyr Ala Thr Arg Leu Gln Asp
 305 35 40 45
 308 Leu Arg Val Thr Phe His Arg Val Lys Pro Thr Leu Val Gly His Val

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309 50 55 60
312 Gly Thr Val Tyr Cys Asp Gly Leu Ser Phe Pro Arg Val Gly
313 65 70 75
316 <210> SEQ ID NO: 19
317 <211> LENGTH: 178
318 <212> TYPE: PRT
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 19
323 Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
324 1 5 10 15
327 Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
328 20 25 30
331 Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
332 35 40 45
335 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
336 50 55 60
339 Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
340 65 70 75 80
343 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
344 85 90 95
347 Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
348 100 105 110
351 Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
352 115 120 125
355 Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
356 130 135 140
359 Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
360 145 150 155 160
363 Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
364 165 170 175
367 Arg Asn
371 <210> SEQ ID NO: 20
372 <211> LENGTH: 160
373 <212> TYPE: PRT
374 <213> ORGANISM: Epstein-Barr virus
376 <400> SEQUENCE: 20
378 Met Glu Arg Arg Leu Val Val Thr Leu Gln Cys Leu Val Leu Leu Tyr
379 1 5 10 15
382 Leu Ala Pro Glu Cys Gly Gly Thr Asp Gln Cys Asp Asn Phe Pro Gln
383 20 25 30
386 Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
387 35 40 45
390 Gln Thr Lys Asp Glu Val Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
391 50 55 60
394 Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile
395 65 70 75 80
398 Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro
399 85 90 95
402 Glu Ala Lys Asp His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu

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